

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/787,091DATE: 03/13/97
TIME: 11:04:32

INPUT SET: S16170.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

- 1
2
3 (1) General Information:
4
5 (i) APPLICANT: Carpino, Nicholas A.
6 Kobayashi, Ryuji
7 Wisniewski, David G.
8 Strife, Annabel O'C.
9 Clarkson, Bayard D.
10
11 (ii) TITLE OF INVENTION: A Novel Human Gene/Protein Involved in
12 Chronic Myelogenous Leukemia
13
14 (iii) NUMBER OF SEQUENCES: 20
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
18 (B) STREET: Two Militia Drive
19 (C) CITY: Lexington
20 (D) STATE: MA
21 (E) COUNTRY: US
22 (F) ZIP: 02173
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: US 60/030,418
37 (B) FILING DATE: 01-NOV-1996
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Granahan, Patricia
41 (B) REGISTRATION NUMBER: 32,227
42 (C) REFERENCE/DOCKET NUMBER: CSHL96-05pa
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 617-861-6240
46 (B) TELEFAX: 617-861-9540

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/787,091DATE: 03/13/97
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47

48

49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1446 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

56

57 (ii) MOLECULE TYPE: DNA (genomic)

58

59

60 (ix) FEATURE:

61 (A) NAME/KEY: CDS

62 (B) LOCATION: 1..1443

63

64

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

66

67 ATG GAC GGA GCA GTG ATG GAA GGG CCG CTT TTT TTG CAG AGT CAG CGC 48

68 Met Asp Gly Ala Val Met Glu Gly Pro Leu Phe Leu Gln Ser Gln Arg

69 1 5 10 15

70

71 TTT GGG ACC AAG AGG TGG AGG AAG ACC TGG GCC GTG CTC TAC CCG GCC 96

72 Phe Gly Thr Lys Arg Trp Arg Lys Thr Trp Ala Val Leu Tyr Pro Ala

73 20 25 30

74

75 AGT CCC CAC GGC GTA GCG CGG CTC GAG TTC TTT GAC CAT AAG GGG TCG 144

76 Ser Pro His Gly Val Ala Arg Leu Glu Phe Phe Asp His Lys Gly Ser

77 35 40 45

78

79 AGC TCT GGG GGT GGC CGA GGG AGC TCG CGC CGC CTG GAC TGC AAA GTG 192

80 Ser Ser Gly Gly Gly Arg Gly Ser Ser Arg Arg Leu Asp Cys Lys Val

81 50 55 60

82

83 ATC CGT CTG GCT GAG TGT GTG AGT GTG GCC CCC GTC ACC GTG GAG ACC 240

84 Ile Arg Leu Ala Glu Cys Val Ser Val Ala Pro Val Thr Val Glu Thr

85 65 70 75 80

86

87 CCC CCT GAG CCC GGC GCC ACT GCC TTC CGC CTG GAC ACT GCT CAG CGC 288

88 Pro Pro Glu Pro Gly Ala Thr Ala Phe Arg Leu Asp Thr Ala Gln Arg

89 85 90 95

90

91 TCG CAC CTG CTG GCG GCC GAC GCG CCG TCC AGT GCA GCC TGG GTG CAG 336

92 Ser His Leu Leu Ala Ala Asp Ala Pro Ser Ser Ala Ala Trp Val Gln

93 100 105 110

94

95 ACG CTG TGC CGA AAC GCC TTT CCG AAA GGC AGC TGG ACT CTG GCG CCT 384

96 Thr Leu Cys Arg Asn Ala Phe Pro Lys Gly Ser Trp Thr Leu Ala Pro

97 115 120 125

98

99 ACC GAT AAC CCA CCT AAG CTT TCT GCC CTG GAG ATG CTG GAG AAC TCC 432

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100	Thr	Asp	Asn	Pro	Pro	Lys	Leu	Ser	Ala	Leu	Glu	Met	Leu	Glu	Asn	Ser	
101		130					135					140					
102																	
103	TTG	TAC	AGC	CCT	ACC	TGG	GAA	GGA	TCC	CAA	TTC	TGG	GTA	ACG	GTG	CAG	480
104	Leu	Tyr	Ser	Pro	Thr	Trp	Glu	Gly	Ser	Gln	Phe	Trp	Val	Thr	Val	Gln	
105	145					150					155					160	
106																	
107	AGG	ACT	GAG	GCC	GCC	GAG	CGC	TGT	GGC	CTG	CAT	GGC	TCC	TAC	GTG	CTG	528
108	Arg	Thr	Glu	Ala	Ala	Glu	Arg	Cys	Gly	Leu	His	Gly	Ser	Tyr	Val	Leu	
109				165						170					175		
110																	
111	AGG	GTG	GAG	GCT	GAA	AGG	CTG	ACT	CTC	CTG	ACC	GTG	GGG	GCC	CAG	AGT	576
112	Arg	Val	Glu	Ala	Glu	Arg	Leu	Thr	Leu	Leu	Thr	Val	Gly	Ala	Gln	Ser	
113				180					185					190			
114																	
115	CAG	ATA	CTG	GAG	CCA	CTC	CTG	TCC	TGG	CCC	TAC	ACT	CTG	TTG	CGT	CGC	624
116	Gln	Ile	Leu	Glu	Pro	Leu	Leu	Ser	Trp	Pro	Tyr	Thr	Leu	Leu	Arg	Arg	
117			195					200					205				
118																	
119	TAT	GGC	CGG	GAC	AAG	GTC	ATG	TTC	TCT	TTC	GAG	GCC	GGC	CGC	CGC	TGC	672
120	Tyr	Gly	Arg	Asp	Lys	Val	Met	Phe	Ser	Phe	Glu	Ala	Gly	Arg	Arg	Cys	
121		210					215					220					
122																	
123	CCC	TCA	GGC	CCT	GGA	ACC	TTC	ACC	TTC	CAG	ACG	GCA	CAG	GGA	AAT	GAC	720
124	Pro	Ser	Gly	Pro	Gly	Thr	Phe	Thr	Phe	Gln	Thr	Ala	Gln	Gly	Asn	Asp	
125	225					230					235					240	
126																	
127	ATC	TTC	CAG	GCA	GTT	GAG	ACT	GCC	ATC	CAC	CGG	CAG	AAG	GCC	CAG	GGA	768
128	Ile	Phe	Gln	Ala	Val	Glu	Thr	Ala	Ile	His	Arg	Gln	Lys	Ala	Gln	Gly	
129				245						250					255		
130																	
131	AAG	GCC	GGA	CAG	GGG	CAC	GAT	GTT	CTC	AGA	GCT	GAC	TCC	CAT	GAA	GGG	816
132	Lys	Ala	Gly	Gln	Gly	His	Asp	Val	Leu	Arg	Ala	Asp	Ser	His	Glu	Gly	
133				260					265					270			
134																	
135	GAG	GTG	GCA	GAG	GGG	AAG	TTG	CCT	TCC	CCA	CCT	GGC	CCC	CAA	GAG	CTC	864
136	Glu	Val	Ala	Glu	Gly	Lys	Leu	Pro	Ser	Pro	Pro	Gly	Pro	Gln	Glu	Leu	
137			275					280					285				
138																	
139	CTC	GAC	AGT	CCC	CCA	GCC	CTG	TAT	GCT	GAG	CCC	TTA	GAC	TCC	CTG	CGC	912
140	Leu	Asp	Ser	Pro	Pro	Ala	Leu	Tyr	Ala	Glu	Pro	Leu	Asp	Ser	Leu	Arg	
141		290					295					300					
142																	
143	ATT	GCT	CCA	TGC	CCT	TCC	CAG	GAC	TCC	CTA	TAC	TCA	GAC	CCC	TTG	GAC	960
144	Ile	Ala	Pro	Cys	Pro	Ser	Gln	Asp	Ser	Leu	Tyr	Ser	Asp	Pro	Leu	Asp	
145	305					310					315				320		
146																	
147	AGC	ACG	TCT	GCT	CAG	GCA	GGA	GAG	GGA	GTA	CAA	CGG	AAG	AAA	CCT	CTC	1008
148	Ser	Thr	Ser	Ala	Gln	Ala	Gly	Glu	Gly	Val	Gln	Arg	Lys	Lys	Pro	Leu	
149				325						330					335		
150																	
151	TAT	TGG	GAC	TTG	TAT	GAG	CAT	GCG	CAG	CAG	CAG	TTG	CTG	AAG	GCC	AAG	1056
152	Tyr	Trp	Asp	Leu	Tyr	Glu	His	Ala	Gln	Gln	Gln	Leu	Leu	Lys	Ala	Lys	

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153		340		345		350	
154							
155	CTG ACA GAC CCC AAA GAG GAT CCC ATC TAT GAT GAA CCT GAG GGC CTG						1104
156	Leu Thr Asp Pro Lys Glu Asp Pro Ile Tyr Asp Glu Pro Glu Gly Leu						
157	355		360		365		
158							
159	GCC CCA GTC CCT CCC CAG GGC CTT TAT GAT CTG CCT CGG GAG CCC AAG						1152
160	Ala Pro Val Pro Pro Gln Gly Leu Tyr Asp Leu Pro Arg Glu Pro Lys						
161	370		375		380		
162							
163	GAT GCA TGG TGG TGC CAA GCT CGG GTG AAG GAG GAG GGC TAT GAG CTC						1200
164	Asp Ala Trp Trp Cys Gln Ala Arg Val Lys Glu Glu Gly Tyr Glu Leu						
165	385		390		395		400
166							
167	CCC TAC AAC CCT GCC ACT GAT GAC TAC GCT GTG CCA CCC CCT CGG AGC						1248
168	Pro Tyr Asn Pro Ala Thr Asp Asp Tyr Ala Val Pro Pro Pro Arg Ser						
169	405		410		415		
170							
171	ACA AAG CCC CTC CTT GCT CCC AAG CCC CAG GGC CCA GCC TTC CCT GAA						1296
172	Thr Lys Pro Leu Leu Ala Pro Lys Pro Gln Gly Pro Ala Phe Pro Glu						
173	420		425		430		
174							
175	CCT GGT ACT GCA ACT GGC AGT GGC ATC AAA AGC CAC AAC TCA GCC CTG						1344
176	Pro Gly Thr Ala Thr Gly Ser Gly Ile Lys Ser His Asn Ser Ala Leu						
177	435		440		445		
178							
179	TAC AGC CAG GTC CAG AAG AGC GGG GCC TCA GGG AGC TGG GAC TGT GGG						1392
180	Tyr Ser Gln Val Gln Lys Ser Gly Ala Ser Gly Ser Trp Asp Cys Gly						
181	450		455		460		
182							
183	CTC TCT AGA GTA GGG ACT GAC AAG ACT GGG GTC AAG TCA GAG GGC TCT						1440
184	Leu Ser Arg Val Gly Thr Asp Lys Thr Gly Val Lys Ser Glu Gly Ser						
185	465		470		475		480
186							
187	ACC TGA						1446
188	Thr						
189							
190							
191							
192	(2) INFORMATION FOR SEQ ID NO:2:						
193							
194	(i) SEQUENCE CHARACTERISTICS:						
195	(A) LENGTH: 481 amino acids						
196	(B) TYPE: amino acid						
197	(D) TOPOLOGY: linear						
198							
199	(ii) MOLECULE TYPE: protein						
200							
201	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:						
202							
203	Met Asp Gly Ala Val Met Glu Gly Pro Leu Phe Leu Gln Ser Gln Arg						
204	1	5	10	15			
205							

RAW SEQUENCE LISTING PATENT APPLICATION US/08/787,091

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206	Phe	Gly	Thr	Lys	Arg	Trp	Arg	Lys	Thr	Trp	Ala	Val	Leu	Tyr	Pro	Ala
207				20					25					30		
208																
209	Ser	Pro	His	Gly	Val	Ala	Arg	Leu	Glu	Phe	Phe	Asp	His	Lys	Gly	Ser
210			35					40					45			
211																
212	Ser	Ser	Gly	Gly	Gly	Arg	Gly	Ser	Ser	Arg	Arg	Leu	Asp	Cys	Lys	Val
213		50					55					60				
214																
215	Ile	Arg	Leu	Ala	Glu	Cys	Val	Ser	Val	Ala	Pro	Val	Thr	Val	Glu	Thr
216	65					70					75				80	
217																
218	Pro	Pro	Glu	Pro	Gly	Ala	Thr	Ala	Phe	Arg	Leu	Asp	Thr	Ala	Gln	Arg
219					85					90					95	
220																
221	Ser	His	Leu	Leu	Ala	Ala	Asp	Ala	Pro	Ser	Ser	Ala	Ala	Trp	Val	Gln
222				100					105					110		
223																
224	Thr	Leu	Cys	Arg	Asn	Ala	Phe	Pro	Lys	Gly	Ser	Trp	Thr	Leu	Ala	Pro
225			115						120				125			
226																
227	Thr	Asp	Asn	Pro	Pro	Lys	Leu	Ser	Ala	Leu	Glu	Met	Leu	Glu	Asn	Ser
228		130					135					140				
229																
230	Leu	Tyr	Ser	Pro	Thr	Trp	Glu	Gly	Ser	Gln	Phe	Trp	Val	Thr	Val	Gln
231	145					150					155				160	
232																
233	Arg	Thr	Glu	Ala	Ala	Glu	Arg	Cys	Gly	Leu	His	Gly	Ser	Tyr	Val	Leu
234				165						170					175	
235																
236	Arg	Val	Glu	Ala	Glu	Arg	Leu	Thr	Leu	Leu	Thr	Val	Gly	Ala	Gln	Ser
237			180						185					190		
238																
239	Gln	Ile	Leu	Glu	Pro	Leu	Leu	Ser	Trp	Pro	Tyr	Thr	Leu	Leu	Arg	Arg
240			195					200					205			
241																
242	Tyr	Gly	Arg	Asp	Lys	Val	Met	Phe	Ser	Phe	Glu	Ala	Gly	Arg	Arg	Cys
243		210					215					220				
244																
245	Pro	Ser	Gly	Pro	Gly	Thr	Phe	Thr	Phe	Gln	Thr	Ala	Gln	Gly	Asn	Asp
246	225					230					235				240	
247																
248	Ile	Phe	Gln	Ala	Val	Glu	Thr	Ala	Ile	His	Arg	Gln	Lys	Ala	Gln	Gly
249				245						250					255	
250																
251	Lys	Ala	Gly	Gln	Gly	His	Asp	Val	Leu	Arg	Ala	Asp	Ser	His	Glu	Gly
252			260						265					270		
253																
254	Glu	Val	Ala	Glu	Gly	Lys	Leu	Pro	Ser	Pro	Pro	Gly	Pro	Gln	Glu	Leu
255			275					280					285			
256																
257	Leu	Asp	Ser	Pro	Pro	Ala	Leu	Tyr	Ala	Glu	Pro	Leu	Asp	Ser	Leu	Arg
258		290					295						300			

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/787,091

DATE: 03/13/97
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Line

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Original Text

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,540DATE: 03/13/97
TIME: 11:02:46

INPUT SET: S16169.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: Huse, William D.
- (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell & Flores LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-IX 2405
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,540DATE: 03/13/97
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47 (D) TOPOLOGY: linear

48

49

50 (ix) FEATURE:

51 (A) NAME/KEY: CDS

52 (B) LOCATION: 1..351

53

54

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

56

57 CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG 48

58 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

59 1 5 10 15

60

61 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96

62 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

63 20 25 30

64

65 GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC 144

66 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

67 35 40 45

68

69 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192

70 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val

71 50 55 60

72

73 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC 240

74 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

75 65 70 75 80

76

77 CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT 288

78 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

79 85 90 95

80

81 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA 336

82 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr

83 100 105 110

84

85 GTG ACT GTT TCT AGT 351

86 Val Thr Val Ser Ser

87 115

88

89

90 (2) INFORMATION FOR SEQ ID NO:2:

91

92 (i) SEQUENCE CHARACTERISTICS:

93 (A) LENGTH: 117 amino acids

94 (B) TYPE: amino acid

95 (D) TOPOLOGY: linear

96

97 (ii) MOLECULE TYPE: protein

98

99 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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100
101 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
102 1 5 10 15
103
104 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
105 20 25 30
106
107 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
108 35 40 45
109
110 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
111 50 55 60
112
113 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
114 65 70 75 80
115
116 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
117 85 90 95
118
119 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
120 100 105 110
121
122 Val Thr Val Ser Ser
123 115
124

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(2) INFORMATION FOR SEQ ID NO:3:

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127 (i) SEQUENCE CHARACTERISTICS:
128 (A) LENGTH: 321 base pairs
129 (B) TYPE: nucleic acid
130 (C) STRANDEDNESS: single
131 (D) TOPOLOGY: linear
132

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```

134 (ix) FEATURE:
135 (A) NAME/KEY: CDS
136 (B) LOCATION: 1..321
137

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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140
141 GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA 48
142 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
143 1 5 10 15
144
145 GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC 96
146 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
147 20 25 30
148
149 CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC 144
150 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
151 35 40 45
152

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/790,540

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153 MKK TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC      192
154 Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
155      50                      55                      60
156
157 AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT      240
158 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
159      65                      70                      75                      80
160
161 GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
162 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
163                      85                      90                      95
164
165 ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG      321
166 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
167      100                      105
168
169

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

180
181 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
182      1                      5                      10                      15
183
184 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
185      20                      25                      30
186
187 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
188      35                      40                      45
189
190 Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
191      50                      55                      60
192
193 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
194      65                      70                      75                      80
195
196 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
197      85                      90                      95
198
199 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
200      100                      105
201

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

RAW SEQUENCE LISTING
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206 (B) TYPE: nucleic acid
207 (C) STRANDEDNESS: single
208 (D) TOPOLOGY: linear
209
210

211 (ix) FEATURE:

212 (A) NAME/KEY: CDS
213 (B) LOCATION: 1..351
214
215

216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

217
218 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG 48
219 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
220 1 5 10 15
221
222 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT 96
223 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
224 20 25 30
225
226 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC 144
227 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
228 35 40 45
229
230 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192
231 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
232 50 55 60
233
234 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC 240
235 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
236 65 70 75 80
237
238 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT 288
239 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
240 85 90 95
241
242 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG 336
243 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
244 100 105 110
245
246 GTC ACT GTC TCT GCA 351
247 Val Thr Val Ser Ala
248 115
249
250

251 (2) INFORMATION FOR SEQ ID NO:6:

252 (i) SEQUENCE CHARACTERISTICS:

253 (A) LENGTH: 117 amino acids
254 (B) TYPE: amino acid
255 (D) TOPOLOGY: linear
256
257

258 (ii) MOLECULE TYPE: protein

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/790,540

DATE: 03/13/97
TIME: 11:02:57

INPUT SET: S16169.raw

Line

Error

Original Text